

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/706,243

DATE: 07/17/2001

TIME: 11:04:45

Input Set : N:\Crf3\RULE60\09229037.txt

Output Set: N:\CRF3\07172001\I706243.raw

ENTERED

3 <110> APPLICANT: Cox III, George Norbert
 4 Case, Casey Christopher
 5 Eisenberg, Stephen P.
 6 Jarvis, Eric Edward
 7 Spratt, Sharon Kaye
 8 Sangamo Biosciences, Inc.

10 <120> TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
 11 Zinc Finger Proteins

13 <130> FILE REFERENCE: 019496-002200US

15 <140> CURRENT APPLICATION NUMBER: 09/706,243

16 <141> CURRENT FILING DATE: 2000-11-03

18 <150> PRIOR APPLICATION NUMBER: 09/229,037

19 <151> PRIOR FILING DATE: 1999-01-12

21 <160> NUMBER OF SEQ ID NOS: 40

23 <170> SOFTWARE: PatentIn Ver. 2.0

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 25

27 <212> TYPE: PRT

28 <213> ORGANISM: Artificial Sequence

30 <220> FEATURE:

31 <223> OTHER INFORMATION: Description of Artificial Sequence:exemplary motif
 32 of C2H2 class of zinc finger proteins (ZFP)

34 <220> FEATURE:

35 <221> NAME/KEY: MOD_RES

36 <222> LOCATION: (2)..(3)

37 <223> OTHER INFORMATION: Xaa = any amino acid

39 <220> FEATURE:

40 <221> NAME/KEY: MOD_RES

41 <222> LOCATION: (4)..(5)

42 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent

44 <220> FEATURE:

45 <221> NAME/KEY: MOD_RES

46 <222> LOCATION: (7)..(18)

47 <223> OTHER INFORMATION: Xaa = any amino acid

49 <220> FEATURE:

50 <221> NAME/KEY: MOD_RES

51 <222> LOCATION: (20)..(22)

52 <223> OTHER INFORMATION: Xaa = any amino acid

54 <220> FEATURE:

55 <221> NAME/KEY: MOD_RES

56 <222> LOCATION: (23)..(24)

57 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent

59 <400> SEQUENCE: 1

W--> 60 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 61 1 5 10 15

W--> 63 Xaa Xaa His Xaa Xaa Xaa Xaa His
 64 20 25

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67 <210> SEQ ID NO: 2
68 <211> LENGTH: 10
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
74     with two overlapping D-able subsites
76 <220> FEATURE:
77 <221> NAME/KEY: modified_base
78 <222> LOCATION: (1)..(2)
79 <223> OTHER INFORMATION: n = g,a,c or t
81 <220> FEATURE:
82 <221> NAME/KEY: modified_base
83 <222> LOCATION: (5)
84 <223> OTHER INFORMATION: n = g,a,c or t
86 <220> FEATURE:
87 <221> NAME/KEY: modified_base
88 <222> LOCATION: (8)
89 <223> OTHER INFORMATION: n = g,a,c or t
91 <220> FEATURE:
92 <221> NAME/KEY: modified_base
93 <222> LOCATION: (9)
94 <223> OTHER INFORMATION: n = a,c or t; if g, then position 10 cannot be g
95     or t
97 <220> FEATURE:
98 <221> NAME/KEY: modified_base
99 <222> LOCATION: (10)
100 <223> OTHER INFORMATION: n = a or c; if g or t, then position 9 cannot be g
102 <400> SEQUENCE: 2
W--> 103 nngkngknnn 10
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 10
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
113     with three overlapping D-able subsites
115 <220> FEATURE:
116 <221> NAME/KEY: modified_base
117 <222> LOCATION: (1)..(2)
118 <223> OTHER INFORMATION: n = g,a,c or t
120 <220> FEATURE:
121 <221> NAME/KEY: modified_base
122 <222> LOCATION: (5)
123 <223> OTHER INFORMATION: n = g,a,c or t
125 <220> FEATURE:
126 <221> NAME/KEY: modified_base
127 <222> LOCATION: (8)
128 <223> OTHER INFORMATION: n = g,a,c or t

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130 <400> SEQUENCE: 3
W--> 131 nngkngkngk 10
134 <210> SEQ ID NO: 4
135 <211> LENGTH: 5
136 <212> TYPE: PRT
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
142 <400> SEQUENCE: 4
143 Asp Gly Gly Gly Ser
144 1 5
147 <210> SEQ ID NO: 5
148 <211> LENGTH: 5
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
155 <400> SEQUENCE: 5
156 Thr Gly Glu Lys Pro
157 1 5
160 <210> SEQ ID NO: 6
161 <211> LENGTH: 9
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
168 <400> SEQUENCE: 6
169 Leu Arg Gln Lys Asp Gly Glu Arg Pro
170 1 5
173 <210> SEQ ID NO: 7
174 <211> LENGTH: 4
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
181 <400> SEQUENCE: 7
182 Gly Gly Arg Arg
183 1
186 <210> SEQ ID NO: 8
187 <211> LENGTH: 5
188 <212> TYPE: PRT
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
194 <400> SEQUENCE: 8
195 Gly Gly Gly Gly Ser
196 1 5
199 <210> SEQ ID NO: 9
200 <211> LENGTH: 8

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201 <212> TYPE: PRT
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
207 <400> SEQUENCE: 9
208 Gly Gly Arg Arg Gly Gly Gly Ser
209   1           5
212 <210> SEQ ID NO: 10
213 <211> LENGTH: 9
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
220 <400> SEQUENCE: 10
221 Leu Arg Gln Arg Asp Gly Glu Arg Pro
222   1           5
225 <210> SEQ ID NO: 11
226 <211> LENGTH: 12
227 <212> TYPE: PRT
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
233 <400> SEQUENCE: 11
234 Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
235   1           5           10
238 <210> SEQ ID NO: 12
239 <211> LENGTH: 16
240 <212> TYPE: PRT
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
246 <400> SEQUENCE: 12
247 Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
248   1           5           10           15
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 25
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
258     region surrounding initiation site of vascular
259     endothelial growth factor (VEGF) gene containing
260     two 9-base pair target sites
262 <220> FEATURE:
263 <221> NAME/KEY: protein_bind
264 <222> LOCATION: (4)..(12)
265 <223> OTHER INFORMATION: upstream 9-base pair ZFP VEGF1 target site
267 <220> FEATURE:
268 <221> NAME/KEY: protein_bind

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269 <222> LOCATION: (14)..(22)
270 <223> OTHER INFORMATION: downstream 9-base pair ZFP VEGF3a target site
272 <400> SEQUENCE: 13
273 agcggggagg atcgcggagg cttgg 25
276 <210> SEQ ID NO: 14
277 <211> LENGTH: 298
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
283     construct targeting upstream 9-base pair target
284     site in VEGF promoter
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (2)..(298)
289 <223> OTHER INFORMATION: VEGF1
291 <400> SEQUENCE: 14
292 g gta ccc ata cct ggc aag aag aag cag cac atc tgc cac atc cag ggc 49
293   Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
294     1           5           10           15
296 tgt ggt aaa gtt tac ggc aca acc tca aat ctg cgt cgt cac ctg cgc 97
297 Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg
298     20           25           30
300 tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt 145
301 Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
302     35           40           45
304 aaa cgc ttc acc cgt tgc tca aac ctg cag cgt cac aag cgt acc cac 193
305 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
306     50           55           60
308 acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg 241
309 Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
310     65           70           75           80
312 cgt agt gac cac ctg tcc cgt cac atc aag acc cac cag aat aag aag 289
313 Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
314     85           90           95
316 ggt gga tcc 298
317 Gly Gly Ser
320 <210> SEQ ID NO: 15
321 <211> LENGTH: 99
322 <212> TYPE: PRT
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
327     construct targeting upstream 9-base pair target
328     site in VEGF promoter
330 <400> SEQUENCE: 15
331 Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
332     1           5           10           15
334 Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09229037.txt

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L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3